

# SEQUENCE LISTING

## (1) GENERAL INFORMATION:

- (i) APPLICANT: Feder, John N.  
Bjorkman, Pamela J.  
Schatzman, Randall C.
- (ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR  
DIAGNOSIS AND TREATMENT OF IRON OVERLOAD DISEASES  
AND IRON DEFICIENCY DISEASES
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Pennie & Edmonds, LLP  
(B) STREET: 1155 Avenue of the Americas  
(C) CITY: New York  
(D) STATE: NY  
(E) COUNTRY: USA  
(F) ZIP: 10036-2811
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: Windows  
(D) SOFTWARE: FastSEQ for Windows Version 2.0b
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: to be assigned  
(B) FILING DATE: June 12, 1998  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER: 08/876,010  
(B) FILING DATE: June 13, 1997
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Poissant, Brian M  
(B) REGISTRATION NUMBER: 28,462  
(C) REFERENCE/DOCKET NUMBER: 8907-0074-999
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 650-493-4935  
(B) TELEFAX: 650-493-5556  
(C) TELEX: 66141 PENNIE

## (2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 276 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Arg Leu Leu Arg Ser His Ser Leu His Tyr Leu Phe Met Gly Ala Ser  
1 5 10  
Glu Gln Asp Leu Gly Leu Ser Leu Phe Glu Ala Leu Gly Tyr Val Asp

Asp	Gln	Leu	20	Phe	Tyr	Asp	25	Glu	Ser	Arg	Arg	30	Val	Glu	Pro
		35				40					45				
Arg	Thr	Pro	Trp	Val	Ser	Ser	Arg	Ile	Ser	Ser	Gln	Met	Trp	Leu	Gln
		50				55					60				
Leu	Ser	Gln	Ser	Leu	Lys	Gly	Trp	Asp	His	Met	Phe	Thr	Val	Asp	Phe
65					70					75				80	
Trp	Thr	Ile	Met	Glu	Asn	His	Asn	His	Ser	Lys	Glu	Ser	His	Thr	Leu
				85					90					95	
Gln	Val	Ile	Leu	Gly	Cys	Glu	Met	Gln	Glu	Asp	Asn	Ser	Thr	Glu	Gly
			100					105					110		
Tyr	Trp	Lys	Tyr	Gly	Tyr	Asp	Gly	Gln	Asp	His	Leu	Glu	Phe	Cys	Pro
		115					120					125			
Asp	Thr	Leu	Asp	Trp	Arg	Ala	Ala	Glu	Pro	Arg	Ala	Trp	Pro	Thr	Lys
		130				135					140				
Leu	Glu	Trp	Glu	Arg	His	Lys	Ile	Arg	Ala	Arg	Gln	Asn	Arg	Ala	Tyr
145					150					155				160	
Leu	Glu	Arg	Asp	Cys	Pro	Ala	Gln	Leu	Gln	Gln	Leu	Leu	Glu	Leu	Gly
				165					170					175	
Arg	Gly	Val	Leu	Asp	Gln	Gln	Val	Pro	Leu	Val	Lys	Val	Thr	His	
			180					185					190		
His	Val	Thr	Ser	Ser	Val	Thr	Thr	Leu	Arg	Cys	Arg	Ala	Leu	Asn	Tyr
		195						200				205			
Tyr	Pro	Gln	Asn	Ile	Thr	Met	Lys	Trp	Leu	Lys	Asp	Lys	Gln	Pro	Met
		210				215					220				
Asp	Ala	Lys	Glu	Phe	Glu	Pro	Lys	Asp	Val	Leu	Pro	Asn	Gly	Asp	Gly
225					230					235				240	
Thr	Tyr	Gln	Gly	Trp	Ile	Thr	Leu	Ala	Val	Pro	Gly	Glu	Glu	Gln	
				245					250					255	
Arg	Tyr	Thr	Cys	Gln	Val	Glu	His	Pro	Gly	Leu	Asp	Gln	Pro	Leu	Ile
			260					265					270		
Val	Ile	Trp	Glu												
		275													

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Arg	Leu	Leu	Arg	Ser	His	Ser	Leu	His	Tyr	Leu	Phe	Met	Gly	Ala	Ser
1				5					10					15	
Glu	Gln	Asp	Leu	Gly	Leu	Ser	Leu	Phe	Glu	Ala	Leu	Gly	Tyr	Val	Asp
			20					25					30		
Asp	Gln	Leu	Phe	Val	Phe	Tyr	Asp	Asp	Glu	Ser	Arg	Arg	Val	Glu	Pro
			35				40					45			
Arg	Thr	Pro	Trp	Val	Ser	Ser	Arg	Ile	Ser	Ser	Gln	Met	Trp	Leu	Gln
		50				55					60				
Leu	Ser	Gln	Ser	Leu	Lys	Gly	Trp	Asp	His	Met	Phe	Thr	Val	Asp	Phe
65					70					75				80	
Trp	Thr	Ile	Met	Glu	Asn	His	Asn	His	Ser	Lys	Glu	Ser	His	Thr	Leu
				85					90					95	
Gln	Val	Ile	Leu	Gly	Cys	Glu	Met	Gln	Glu	Asp	Asn	Ser	Thr	Glu	Gly
			100					105					110		
Tyr	Trp	Lys	Tyr	Gly	Tyr	Asp	Gly	Gln	Asp	His	Leu	Glu	Phe	Cys	Pro
		115					120					125			
Asp	Thr	Leu	Asp	Trp	Arg	Ala	Ala	Glu	Pro	Arg	Ala	Trp	Pro	Thr	Lys
		130				135					140				
Leu	Glu	Trp	Glu	Arg	His	Lys	Ile	Arg	Ala	Arg	Gln	Asn	Arg	Ala	Tyr
145					150					155				160	
Leu	Glu	Arg	Asp	Cys	Pro	Ala	Gln	Leu	Gln	Gln	Leu	Leu	Glu	Leu	Gly

Arg	Gly	Val	Leu	165	Gln	Gln	Val	Pro	170	Leu	Val	Lys	Val	175	Thr	His
His	Val	Thr	Ser	180	Val	Thr	Thr	Leu	185	Arg	Cys	Arg	Ala	190	Leu	Asn
Tyr	Pro	Gln	Asn	195	Ile	Thr	Met	Lys	200	Trp	Leu	Lys	Asp	205	Gln	Pro
Asp	Ala	Lys	Glu	210	Phe	Glu	Pro	Lys	215	Asp	Val	Leu	Pro	220	Asn	Gly
225	Thr	Tyr	Gln	225	Gly	Trp	Ile	Thr	230	Leu	Ala	Val	Pro	235	Gly	Glu
Thr	Tyr	Gln	Gly	245	Trp	Ile	Thr	Leu	250	Ala	Val	Pro	Pro	255	Gly	Glu
Arg	Tyr	Thr	Cys	260	Gln	Val	Glu	His	265	Pro	Gly	Leu	Asp	270	Gln	Pro
Val	Ile	Trp	Glu	275												

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 276 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Arg	Leu	Leu	Arg	Ser	His	Ser	Leu	His	Tyr	Leu	Phe	Met	Gly	Ala	Ser
1				5					10					15	
Glu	Gln	Asp	Leu	Gly	Leu	Ser	Leu	Phe	Glu	Ala	Leu	Gly	Tyr	Val	Asp
			20					25					30		
Asp	Gln	Leu	Phe	Val	Phe	Tyr	Asp	His	Glu	Ser	Arg	Arg	Val	Glu	Pro
			35					40					45		
Arg	Thr	Pro	Trp	Val	Ser	Ser	Arg	Ile	Ser	Ser	Gln	Met	Trp	Leu	Gln
			50				55					60			
Leu	Ser	Gln	Ser	Leu	Lys	Gly	Trp	Asp	His	Met	Phe	Thr	Val	Asp	Phe
65					70				75					80	
Trp	Thr	Ile	Met	Glu	Asn	His	Asn	Ala	Ser	Lys	Glu	Ser	His	Thr	Leu
				85				90						95	
Gln	Val	Ile	Leu	Gly	Cys	Glu	Met	Gln	Glu	Asp	Asn	Ser	Thr	Glu	Gly
			100					105					110		
Tyr	Trp	Lys	Tyr	Gly	Tyr	Asp	Gly	Gln	Asp	Ala	Leu	Glu	Phe	Cys	Pro
			115				120					125			
Asp	Thr	Leu	Asp	Trp	Arg	Ala	Ala	Glu	Pro	Arg	Ala	Trp	Pro	Thr	Lys
			130			135					140				
Leu	Glu	Trp	Glu	Arg	His	Lys	Ile	Arg	Ala	Arg	Gln	Asn	Arg	Ala	Tyr
145					150				155					160	
Leu	Glu	Arg	Asp	Cys	Pro	Ala	Gln	Leu	Gln	Gln	Leu	Leu	Glu	Leu	Gly
			165					170						175	
Arg	Gly	Val	Leu	Asp	Gln	Gln	Val	Pro	Pro	Leu	Val	Lys	Val	Thr	His
			180					185						190	
His	Val	Thr	Ser	Ser	Val	Thr	Thr	Leu	Arg	Cys	Arg	Ala	Leu	Asn	Tyr
			195					200				205			
Tyr	Pro	Gln	Asn	Ile	Thr	Met	Lys	Trp	Leu	Lys	Asp	Lys	Gln	Pro	Met
			210				215					220			
Asp	Ala	Lys	Glu	Phe	Glu	Pro	Lys	Asp	Val	Leu	Pro	Asn	Gly	Asp	Gly
225					230				235					240	
Thr	Tyr	Gln	Gly	Trp	Ile	Thr	Leu	Ala	Val	Pro	Pro	Gly	Glu	Glu	Gln
			245					250						255	
Arg	Tyr	Thr	Cys	Gln	Val	Glu	His	Pro	Gly	Leu	Asp	Gln	Pro	Leu	Ile
			260					265						270	
Val	Ile	Trp	Glu												
			275												

(2) INFORMATION FOR SEQ ID NO:4:

[illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible][illegible]